S. Kaushal

1633

ENTERED

RAW SEQUENCE LISTING   DATE: 05/31/2000
PATENT APPLICATION: US/09/155,327B   TIME: 13:59:31

Input Set : A:\11686.seq2
Output Set: N:\CRF3\05312000\I155327B.raw

```
   3 <110> APPLICANT: AMRAD Operations Pty Ltd
   5 <120> TITLE OF INVENTION: A NOVEL MAMMALIAN GENE, bcl-2, BELONGS TO THE bcl-2
   6        FAMILY OF APOPTOSIS-CONTROLLING GENES
   8 <130> FILE REFERENCE: 2096584
  10 <140> CURRENT APPLICATION NUMBER: 09/155,327B
C--> 11 <141> CURRENT FILING DATE: 1999-03-29
  13 <150> PRIOR APPLICATION NUMBER: PN8965
  14 <151> PRIOR FILING DATE: 1996-03-27
  16 <160> NUMBER OF SEQ ID NOS: 9
  18 <170> SOFTWARE: PatentIn Ver. 2.1
  20 <210> SEQ ID NO: 1
  21 <211> LENGTH: 33
  22 <212> TYPE: DNA
  23 <213> ORGANISM: Mouse
  25 <220> FEATURE:
  26 <221> NAME/KEY: modified_base
  27 <222> LOCATION: 16
  28 <223> OTHER INFORMATION: n is inosine
  30 <220> FEATURE:
  31 <221> NAME/KEY: modified_base
  32 <222> LOCATION: 19
  33 <223> OTHER INFORMATION: n is inosine
  35 <220> FEATURE:
  36 <221> NAME/KEY: modified_base
  37 <222> LOCATION: 22
  38 <223> OTHER INFORMATION: n is inosine
  40 <220> FEATURE:
  41 <221> NAME/KEY: modified_base
  42 <222> LOCATION: 25
  43 <223> OTHER INFORMATION: n is inosine
  45 <400> SEQUENCE: 1
  46    gctctagaac tggggnhgnr tngtngcctt ytt                        33
  49 <210> SEQ ID NO: 2
  50 <211> LENGTH: 9
  51 <212> TYPE: PRT
  52 <213> ORGANISM: Mouse
  54 <220> FEATURE:
  55 <221> NAME/KEY: Unsure
  56 <222> LOCATION: 5
  57 <223> OTHER INFORMATION: Xaa is Ile or Val
  59 <400> SEQUENCE: 2
  60    Asn Trp Gly Arg Xaa Val Ala Phe Phe
  61     1                   5
  64 <210> SEQ ID NO: 3
  65 <211> LENGTH: 31
  66 <212> TYPE: DNA
  67 <213> ORGANISM: Mouse
```

RAW SEQUENCE LISTING   DATE: 05/31/2000
PATENT APPLICATION: US/09/155,327B   TIME: 13:59:31

Input Set : A:\11686.seq2
Output Set: N:\CRF3\05312000\I155327B.raw

```
 69 <220> FEATURE:
 70 <221> NAME/KEY: modified_base
 71 <222> LOCATION: 14
 72 <223> OTHER INFORMATION: n is inosine
 74 <220> FEATURE:
 75 <221> NAME/KEY: modified_base
 76 <222> LOCATION: 17
 77 <223> OTHER INFORMATION: n is inosine
 79 <220> FEATURE:
 80 <221> NAME/KEY: modified_base
 81 <222> LOCATION: 20
 82 <223> OTHER INFORMATION: n is inosine
 84 <400> SEQUENCE: 3
 85   ggaattccca gccnccntkn tcttggatcc a                     31
 88 <210> SEQ ID NO: 4
 89 <211> LENGTH: 8
 90 <212> TYPE: PRT
 91 <213> ORGANISM: Mouse
 93 <220> FEATURE:
 94 <221> NAME/KEY: Unsure
 95 <222> LOCATION: 4
 96 <223> OTHER INFORMATION: Xaa is Asp or Glu
 98 <220> FEATURE:
 99 <221> NAME/KEY: Unsure
100 <222> LOCATION: 5
101 <223> OTHER INFORMATION: Xaa is Asn or Gln
103 <400> SEQUENCE: 4
104   Trp Ile Gln Xaa Xaa Gly Gly Trp
105    1               5
108 <210> SEQ ID NO: 5
109 <211> LENGTH: 14
110 <212> TYPE: PRT
111 <213> ORGANISM: Mouse
113 <400> SEQUENCE: 5
114   Met Ala Thr Pro Ala Ser Thr Pro Asp Thr Arg Ala Leu Val
115    1               5                   10
118 <210> SEQ ID NO: 6
119 <211> LENGTH: 583
120 <212> TYPE: DNA
121 <213> ORGANISM: HUMAN
123 <220> FEATURE:
124 <221> NAME/KEY: CDS
125 <222> LOCATION: (1)..(579)
127 <400> SEQUENCE: 6
128   atg gcg acc cca gcc tcg gcc cca gac aca cgg gct ctg gtg gca gac   48
129   Met Ala Thr Pro Ala Ser Ala Pro Asp Thr Arg Ala Leu Val Ala Asp
130    1               5                   10                  15
132   ttt gta ggt tat aag ctg agg cag aag ggt tat gtc tgt gga gct ggc   96
133   Phe Val Gly Tyr Lys Leu Arg Gln Lys Gly Tyr Val Cys Gly Ala Gly
```

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/155,327B

DATE: 05/31/2000
TIME: 13:59:31

Input Set : A:\11686.seq2
Output Set: N:\CRF3\05312000\I155327B.raw

```
134                    20                     25                      30
136      ccc ggg gag ggc cca gca gct gac ccg ctg cac caa gcc atg cgg gca      144
137      Pro Gly Glu Gly Pro Ala Ala Asp Pro Leu His Gln Ala Met Arg Ala
138                    35                     40                      45
140      gct gga gat gag ttc gag acc cgc ttc cgg cgc acc ttc tct gat ctg      192
141      Ala Gly Asp Glu Phe Glu Thr Arg Phe Arg Arg Thr Phe Ser Asp Leu
142                    50                     55                      60
144      gcg gct cag ctg cat gtg acc cca ggc tca gcc cag caa cgc ttc acc      240
145      Ala Ala Gln Leu His Val Thr Pro Gly Ser Ala Gln Gln Arg Phe Thr
146      65                    70                     75                      80
148      cag gtc tcc gac gaa ctt ttt caa ggg ggc ccc aac tgg ggc cgc ctt      288
149      Gln Val Ser Asp Glu Leu Phe Gln Gly Gly Pro Asn Trp Gly Arg Leu
150                    85                     90                      95
152      gta gcc ttc ttt ctc ttt ggg gct gca ctg tgt gct gag agt gtc aac      336
153      Val Ala Phe Phe Leu Phe Gly Ala Ala Leu Cys Ala Glu Ser Val Asn
154                    100                    105                     110
156      aag gag atg gaa cca ctg gtg gga caa gtg cag gag tgg atg gtg gcc      384
157      Lys Glu Met Glu Pro Leu Val Gly Gln Val Gln Glu Trp Met Val Ala
158                    115                    120                     125
160      tac ctg gag acg cgg ctg gtc gac tgg atc cac agc agt ggg ggc tgg      432
161      Tyr Leu Glu Thr Arg Leu Val Asp Trp Ile His Ser Ser Gly Gly Trp
162      130                   135                    140
164      gcg gag ttc aca gct cta tac ggg gac ggg gcc ctg gag gag gcg cgg      480
165      Ala Glu Phe Thr Ala Leu Tyr Gly Asp Gly Ala Leu Glu Glu Ala Arg
166      145                   150                    155                     160
168      cgt ctg cgg gag ggg aac tgg gca tca gtg agg aca gtg ctg acg ggg      528
169      Arg Leu Arg Glu Gly Asn Trp Ala Ser Val Arg Thr Val Leu Thr Gly
170                    165                    170                     175
172      gcc gtg gca ctg ggg gcc ctg gta act gta ggg gcc ttt ttt gct agc      576
173      Ala Val Ala Leu Gly Ala Leu Val Thr Val Gly Ala Phe Phe Ala Ser
174                    180                    185                     190
176      aag tgaa                                                              583
177      Lys
180 <210> SEQ ID NO: 7
181 <211> LENGTH: 193
182 <212> TYPE: PRT
183 <213> ORGANISM: HUMAN
185 <400> SEQUENCE: 7
186      Met Ala Thr Pro Ala Ser Ala Pro Asp Thr Arg Ala Leu Val Ala Asp
187      1                5                      10                     15
189      Phe Val Gly Tyr Lys Leu Arg Gln Lys Gly Tyr Val Cys Gly Ala Gly
190                    20                     25                      30
192      Pro Gly Glu Gly Pro Ala Ala Asp Pro Leu His Gln Ala Met Arg Ala
193                    35                     40                      45
195      Ala Gly Asp Glu Phe Glu Thr Arg Phe Arg Arg Thr Phe Ser Asp Leu
196      50                    55                     60
198      Ala Ala Gln Leu His Val Thr Pro Gly Ser Ala Gln Gln Arg Phe Thr
199      65                    70                     75                      80
201      Gln Val Ser Asp Glu Leu Phe Gln Gly Gly Pro Asn Trp Gly Arg Leu
```

```
202                     85              90                  95
204   Val Ala Phe Phe Leu Phe Gly Ala Ala Leu Cys Ala Glu Ser Val Asn
205                100              105                 110
207   Lys Glu Met Glu Pro Leu Val Gly Gln Val Gln Glu Trp Met Val Ala
208             115              120                 125
210   Tyr Leu Glu Thr Arg Leu Val Asp Trp Ile His Ser Ser Gly Gly Trp
211        130              135                 140
213   Ala Glu Phe Thr Ala Leu Tyr Gly Asp Gly Ala Leu Glu Glu Ala Arg
214   145              150                 155                 160
216   Arg Leu Arg Glu Gly Asn Trp Ala Ser Val Arg Thr Val Leu Thr Gly
217                165              170                 175
219   Ala Val Ala Leu Gly Ala Leu Val Thr Val Gly Ala Phe Phe Ala Ser
220             180              185                 190
222   Lys
226   <210> SEQ ID NO: 8
227   <211> LENGTH: 581
228   <212> TYPE: DNA
229   <213> ORGANISM: Mouse
231   <220> FEATURE:
232   <221> NAME/KEY: CDS
233   <222> LOCATION: (1)..(579)
235   <400> SEQUENCE: 8
236    atg ccg acc cca gcc tca acc cca gac aca cgc gct cta gtg gct gac      48
237    Met Pro Thr Pro Ala Ser Thr Pro Asp Thr Arg Ala Leu Val Ala Asp
238     1               5                  10                  15
240     ttt gta ggc tat agg ctg agg cag aag ggt tat gtc tgt gga gct ggg      96
241    Phe Val Gly Tyr Arg Leu Arg Gln Lys Gly Tyr Val Cys Gly Ala Gly
242                 20                  25                  30
244    cct ggg gaa ggc cca gcc gcc gac ccg ctg cac caa gcc atg cgg gct     144
245    Pro Gly Glu Gly Pro Ala Ala Asp Pro Leu His Gln Ala Met Arg Ala
246             35                  40                  45
248    gct gga gac gag ttt gag acc cgt ttc cgc cgc acc ttc tct gac ctg     192
249    Ala Gly Asp Glu Phe Glu Thr Arg Phe Arg Arg Thr Phe Ser Asp Leu
250     50                  55                  60
252    gcc gct cag cta cac gtg acc cca ggc tca gcc cag caa cgc ttc acc     240
253    Ala Ala Gln Leu His Val Thr Pro Gly Ser Ala Gln Gln Arg Phe Thr
254    65                  70                  75                  80
256    cag gtt tcc gac gaa ctt ttc caa ggg ggc cct aac tgg ggc cgt ctt     288
257    Gln Val Ser Asp Glu Leu Phe Gln Gly Gly Pro Asn Trp Gly Arg Leu
258                 85                  90                  95
260    gtg gca ttc ttt gtc ttt ggg gct gcc ctg tgt gct gag agt gtc aac     336
261    Val Ala Phe Phe Val Phe Gly Ala Ala Leu Cys Ala Glu Ser Val Asn
262                100                 105                 110
264    aaa gaa atg gag cct ttg gtg gga caa gtc cag gat tgg atc gtg gcc     384
265    Lys Glu Met Glu Pro Leu Val Gly Gln Val Gln Asp Trp Ile Val Ala
266             115                 120                 125
268    tac ctg gag aca cgt ctg gct gac tgg atc cac agc agt ggc ggc tgg     432
269    Tyr Leu Glu Thr Arg Leu Ala Asp Trp Ile His Ser Ser Gly Gly Trp
270     130                 135                 140
```

```
272    gcg gac ttc aca gct cta tac ggg gac ggg gcc ctg gag gac gca cgg    480
273    Ala Asp Phe Thr Ala Leu Tyr Gly Asp Gly Ala Leu Glu Asp Ala Arg
274    145                 150                 155                 160
276    cgt ctg cgg gag ggc aac tgg gca tga gtg agc aca gtg gtg acg ggg    528
277    Arg Leu Arg Glu Gly Asn Trp Ala Val Ser Thr Val Val Thr Gly Ala
278                    165                 170                 175
280    gcc gtg gca ctg ggg gcc ctg gta act gta ggg gcc ttt ttt gct agc    576
281    Val Ala Leu Gly Ala Leu Val Thr Val Gly Ala Phe Phe Ala Ser Lys
282                    180                 185                 190
284    aag tg                                                            581
288    <210> SEQ ID NO: 9
289    <211> LENGTH: 192
290    <212> TYPE: PRT
291    <213> ORGANISM: Mouse
293    <400> SEQUENCE: 9
294    Met Pro Thr Pro Ala Ser Thr Pro Asp Thr Arg Ala Leu Val Ala Asp
295    1               5                   10                  15
296    Phe Val Gly Tyr Arg Leu Arg Gln Lys Gly Tyr Val Cys Gly Ala Gly
297                    20                  25                  30
298    Pro Gly Glu Gly Pro Ala Ala Asp Pro Leu His Gln Ala Met Arg Ala
299                35                  40                  45
300    Ala Gly Asp Glu Phe Glu Thr Arg Phe Arg Arg Thr Phe Ser Asp Leu
301            50                  55                  60
302    Ala Ala Gln Leu His Val Thr Pro Gly Ser Ala Gln Gln Arg Phe Thr
303    65                  70                  75                  80
304    Gln Val Ser Asp Glu Leu Phe Gln Gly Gly Pro Asn Trp Gly Arg Leu
305                    85                  90                  95
306    Val Ala Phe Phe Val Phe Gly Ala Ala Leu Cys Ala Glu Ser Val Asn
307                    100                 105                 110
308    Lys Glu Met Glu Pro Leu Val Gly Gln Val Gln Asp Trp Ile Val Ala
309            115                 120                 125
310    Tyr Leu Glu Thr Arg Leu Ala Asp Trp Ile His Ser Ser Gly Gly Trp
311            130                 135                 140
312    Ala Asp Phe Thr Ala Leu Tyr Gly Asp Gly Ala Leu Glu Asp Ala Arg
313    145                 150                 155                 160
314    Arg Leu Arg Glu Gly Asn Trp Ala Val Ser Thr Val Val Thr Gly
315                    165                 170                 175
316    Ala Val Ala Leu Gly Ala Leu Val Thr Val Gly Ala Phe Phe Ala Ser
317                    180                 185                 190
318    Lys
```

VERIFICATION SUMMARY
PATENT APPLICATION: US/09/155,327B

DATE: 05/31/2000
TIME: 13:59:32

Input Set : A:\11686.seq2
Output Set: N:\CRF3\05312000\I155327B.raw

L:11 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:46 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1
L:60 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:2
L:85 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3
L:104 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4